

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Reyes, Gregory R.
Yarbough, Patrice O
Bradley, Daniel W
Krawczynski, Krzysztof Z
Tam, Albert
Fry, Kirk E
- (ii) TITLE OF INVENTION: DNA Sequences of Enterically Transmitted
Non-A/Non-B Hepatitis Viral Agent
- (iii) NUMBER OF SEQUENCES: 20
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Dehlinger & Associates
 - (B) STREET: 350 Cambridge Avenue, Suite 250
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94306
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/128,275
 - (B) FILING DATE: 03-AUG-1998
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/279,823
 - (B) FILING DATE: 25-JUL-1994
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/681,078
 - (B) FILING DATE: 05-APR-1991
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/505,888
 - (B) FILING DATE: 05-APR-1990
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/420,921
 - (B) FILING DATE: 13-OCT-1989
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/367,486
 - (B) FILING DATE: 16-JUN-1989
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/336,672
 - (B) FILING DATE: 11-APR-1989
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/208,997
 - (B) FILING DATE: 17-JUN-1988

(viii) ATTORNEY/AGENT INFORMATION:
 (A) NAME: Petithory, Joanne R.
 (B) REGISTRATION NUMBER: 42,995
 (C) REFERENCE/DOCKET NUMBER: 4600-0183.24

(ix) TELECOMMUNICATION INFORMATION:
 (A) TELEPHONE: (650) 324-0880
 (B) TELEFAX: (650) 324-0960

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1295 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (C) INDIVIDUAL ISOLATE: 1.33 kb EcoRI insert of ET1.1,
 forward sequence

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1293

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 2..1294

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 3..1295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGACCTGTCC CTGTTGCAGC TGTTCTACCA CCCTGCCCCG AGCTCGAACA GGGCCTTCTC	60
TACCTGCCCC AGGAGCTCAC CACCTGTGAT AGTGTCGTAA CATTTGAATT AACAGACATT	120
GTGCACTGCC GCATGGCCGC CCCGAGCCAG CGCAAGGCCG TGCTGTCCAC ACTCGTGGGC	180
CGCTACGGCG GTCGCACAAA GCTCTACAAT GCTTCCCCT CTGATGTTTCG CGACTCTCTC	240
GCCCGTTTTTA TCCCGGCCAT TGGCCCCGTA CAGGTTACAA CTTGTGAATT GTACGAGCTA	300
TGGGAGGCCA TGGTCGAGAA GGGCCAGGAT GGCTCCGCCG TCCTTGAGCT TGATCTTTGC	360
AACCGTGACG TGTCCAGGAT CACCTTCTTC CAGAAAGATT GTAACAAGTT CACCACAGGT	420
GAGACCATTG CCCATGGTAA AGTGGGCCAG GGCATCTCGG CCTGGAGCAA GACCTTCTGC	480
CCCCTCTTTG GCCCTTGGTT CCGCGCTATT GAGAAGGCTA TTCTGGCCCT GCTCCCTCAG	540
GGTGTGTTTT ACGGTGATGC CTTTGATGAC ACCGTCTTCT CGGCGGCTGT GGCCGCAGCA	600

AAGGCATCCA TGGTGTTTGA GAATGACTTT TCTGAGTTTG ACTCCACCCA GAATAACTTT 660
 TCTCTGGGTC TAGAGTGTGC TATTATGGAG GAGTGTGGGA TGCCGCAGTG GCTCATCCGC 720
 CTGTATCACC TTATAAGGTC TGC GTGGATC TTGCAGGCC CGAAGGAGTC TCTGCGAGGG 780
 TTTTGAAGA AACACTCCGG TGAGCCCGGC ACTCTTCTAT GGAATACTGT CTGGAATATG 840
 GCCGTTATTA CCCACTGTTA TGA CTTCGC GATTTTCAGG TGGCTGCCTT TAAAGGTGAT 900
 GATTCGATAG TGCTTTGCAG TGAGTATCGT CAGAGTCCAG GAGCTGCTGT CCTGATCGCC 960
 GGCTGTGGCT TGAAGTTGAA GGTAGATTTC CGCCGATCG GTTGTATGC AGGTGTTGTG 1020
 GTGGCCCCCG GCCTTGGCGC GCTCCCTGAT GTTGTGCGCT TCGCCGGCCG GCTTACCGAG 1080
 AAGAATTGGG GCCCTGGCCC TGAGCGGGCG GAGCAGCTCC GCCTCGCTGT TAGTGATTTC 1140
 CTCCGCAAGC TCACGAATGT AGCTCAGATG TGTGTGGATG TTGTTTCCCG TGTTTATGGG 1200
 GTTTCCTTG GACTCGTTCA TAACCTGATT GGCATGCTAC AGGCTGTTGC TGATGGCAAG 1260
 GCACATTTCA CTGAGTCAGT AAAACCAAGT CTCGA 1295

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 431 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Arg Pro Val Pro Val Ala Ala Val Leu Pro Pro Cys Pro Glu Leu Glu
 1 5 10 15
 Gln Gly Leu Leu Tyr Leu Pro Gln Glu Leu Thr Thr Cys Asp Ser Val
 20 25 30
 Val Thr Phe Glu Leu Thr Asp Ile Val His Cys Arg Met Ala Ala Pro
 35 40 45
 Ser Gln Arg Lys Ala Val Leu Ser Thr Leu Val Gly Arg Tyr Gly Gly
 50 55 60
 Arg Thr Lys Leu Tyr Asn Ala Ser His Ser Asp Val Arg Asp Ser Leu
 65 70 75 80
 Ala Arg Phe Ile Pro Ala Ile Gly Pro Val Gln Val Thr Thr Cys Glu
 85 90 95
 Leu Tyr Glu Leu Val Glu Ala Met Val Glu Lys Gly Gln Asp Gly Ser
 100 105 110
 Ala Val Leu Glu Leu Asp Leu Cys Asn Arg Asp Val Ser Arg Ile Thr
 115 120 125
 Phe Phe Gln Lys Asp Cys Asn Lys Phe Thr Thr Gly Glu Thr Ile Ala
 130 135 140

His Gly Lys Val Gly Gln Gly Ile Ser Ala Trp Ser Lys Thr Phe Cys
 145 150 155 160
 Ala Leu Phe Gly Pro Trp Phe Arg Ala Ile Glu Lys Ala Ile Leu Ala
 165 170 175
 Leu Leu Pro Gln Gly Val Phe Tyr Gly Asp Ala Phe Asp Asp Thr Val
 180 185 190
 Phe Ser Ala Ala Val Ala Ala Ala Lys Ala Ser Met Val Phe Glu Asn
 195 200 205
 Asp Phe Ser Glu Phe Asp Ser Thr Gln Asn Asn Phe Ser Leu Gly Leu
 210 215 220
 Glu Cys Ala Ile Met Glu Glu Cys Gly Met Pro Gln Trp Leu Ile Arg
 225 230 235 240
 Leu Tyr His Leu Ile Arg Ser Ala Trp Ile Leu Gln Ala Pro Lys Glu
 245 250 255
 Ser Leu Arg Gly Phe Trp Lys Lys His Ser Gly Glu Pro Gly Thr Leu
 260 265 270
 Leu Trp Asn Thr Val Trp Asn Met Ala Val Ile Thr His Cys Tyr Asp
 275 280 285
 Phe Arg Asp Phe Gln Val Ala Ala Phe Lys Gly Asp Asp Ser Ile Val
 290 295 300
 Leu Cys Ser Glu Tyr Arg Gln Ser Pro Gly Ala Ala Val Leu Ile Ala
 305 310 315 320
 Gly Cys Gly Leu Lys Leu Lys Val Asp Phe Arg Pro Ile Gly Leu Tyr
 325 330 335
 Ala Gly Val Val Val Ala Pro Gly Leu Gly Ala Leu Pro Asp Val Val
 340 345 350
 Arg Phe Ala Gly Arg Leu Thr Glu Lys Asn Trp Gly Pro Gly Pro Glu
 355 360 365
 Arg Ala Glu Gln Leu Arg Leu Ala Val Ser Asp Phe Leu Arg Lys Leu
 370 375 380
 Thr Asn Val Ala Gln Met Cys Val Asp Val Val Ser Arg Val Tyr Gly
 385 390 395 400
 Val Ser Pro Gly Leu Val His Asn Leu Ile Gly Met Leu Gln Ala Val
 405 410 415
 Ala Asp Gly Lys Ala His Phe Thr Glu Ser Val Lys Pro Val Leu
 420 425 430

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: linker - top (5') sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGAATTCGCG GCCGCTCG

18

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: linker - bottom (3') sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGAGCGGCCG CGAATTCCTT

20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1295 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: 1.33 kb EcoRI insert of ET1.1,
reverse sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCGAGCACTG GTTTTACTGA CTCAGTGAA TGTGCCTTGC CATCAGCAAC AGCCTGTAGC

60

ATGCCAATCA GGTTATGAAC GAGTCCAGGG GAAACCCCAT AAACACGGGA AACACATCC

120

ACACACATCT GAGCTACATT CGTGAGCTTG CGGAGGAAAT CACTAACAGC GAGGCGGAGC	180
TGCTCCGCCC GCTCAGGGCC AGGGCCCCAA TTCTTCTCGG TAAGCCGGCC GGCGAAGCGC	240
ACAACATCAG GGAGCGCGCC AAGGCCGGGG GCCACCACAA CACCTGCATA CAAACCGATC	300
GGGCGGAAAT CTACCTTCAA CTTCAAGCCA CAGCCGGCGA TCAGGACAGC AGCTCCTGGA	360
CTCTGACGAT ACTCACTGCA AAGCACTATC GAATCATCAC CTTTAAAGGC AGCCACCTGA	420
AAATCGCGGA AGTCATAACA GTGGGTAATA ACGGCCATAT TCCAGACAGT ATTCCATAGA	480
AGAGTGCCGG GCTCACCGBA GTGTTTCTTC CAAAACCCTC GCAGAGACTC CTTGCGGGCC	540
TGCAAGATCC ACGCAGACCT TATAAGGTGA TACAGGCGGA TGAGCCACTG CGGCATCCCA	600
CACTCCTCCA TAATAGCACA CTCTAGACCC AGAGAAAAGT TATTCTGGGT GGAGTCAAAC	660
TCAGAAAAGT CATTCTCAA CACCATGGAT GCCTTTGCTG CGGCCACAGC CGCCGAGAAG	720
ACGGTGTCT CAAAGGCATC ACCGTAAAAC ACACCCTGAG GGAGCAGGGC CAGAATAGCC	780
TTCTCAATAG CGCGGAACCA AGGGCCAAAG AGGGCGCAGA AGGTCTTGCT CCAGGCCGAG	840
ATGCCCTGGC CCACTTTACC ATGGGCAATG GTCTCACCTG TGGTGAACCT GTTACAATCT	900
TTCTGGAAGA AGGTGATCCT GGACACGTCA CGGTTGCAA GATCAAGCTC AAGGACGGCG	960
GAGCCATCCT GGCCCTTCTC GACCATGGCC TCCACTAGCT CGTACAATTC ACAAGTTGTA	1020
ACCTGTACGG GGCCAATGGC CGGGATAAAA CGGGCGAGAG AGTCGCGAAC ATCAGAGTGG	1080
GAAGCATTGT AGAGCTTTGT GCGACCGCCG TAGCGGCCCA CGAGTGTGGA CAGCACGGCC	1140
TTGCGCTGGC TCGGGGCGGC CATGCGGCAG TGCACAATGT CTGTTAATTC AAATGTTACG	1200
ACACTATCAC AGGTGGTGAG CTCCTGGGGC AGGTAGAGAA GGCCCTGTTC GAGCTCGGGG	1260
CAGGGTGGA GAACAGCTGC AACAGGGACA GGTCT	1295

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HEV - Burma strain

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 28..5106

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 5147..7126

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 5106..5474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGGCAGACCA CATATGTGGT CGATGCCATG GAGGCCCATC AGTTTATTAA GGCTCCTGGC	60
ATCACTACTG CTATTGAGCA GGCTGCTCTA GCAGCGGCCA ACTCTGCCCT GGCGAATGCT	120
GTGGTAGTTA GGCCTTTTCT CTCTCACCAG CAGATTGAGA TCCTCATTA CCTAATGCAA	180
CCTCGCCAGC TTGTTTTCCG CCCCAGGTT TTCTGGAATC ATCCCATCCA GCGTGTATC	240
CATAACGAGC TGGAGCTTTA CTGCCGCGCC CGCTCCGGCC GCTGTCTTGA AATTGGCGCC	300
CATCCCCGCT CAATAAATGA TAATCCTAAT GTGGTCCACC GCTGCTTCCT CCGCCCTGTT	360
GGGCGTGATG TTCAGCGCTG GTATACTGCT CCCACTCGCG GGCCGGCTGC TAATTGCCGG	420
CGTTCCGCGC TGC GCGGGCT TCCCCTGCT GACCGCACTT ACTGCCTCGA CGGGTTTTCT	480
GGCTGTAACT TTCCCGCCGA GACTGGCATC GCCCTCTACT CCCTTCATGA TATGTCACCA	540
TCTGATGTCG CCGAGGCCAT GTTCCGCCAT GGTATGACGC GGCTCTATGC CGCCCTCCAT	600
CTTCCGCTG AGGTCCTGCT GCCCCCTGGC ACATATCGCA CCGCATCGTA TTTGCTAATT	660
CATGACGGTA GCGCGTTGT GGTGACGTAT GAGGGTGATA CTAGTGCTGG TTACAACCAC	720
GATGTCTCCA ACTTGCGCTC CTGGATTAGA ACCACCAAGG TTACCGGAGA CCATCCCCTC	780
GTTATCGAGC GGGTTAGGGC CATTTGGCTGC CACTTTGTTC TCTTGCTCAC GGCAGCCCCG	840
GAGCCATCAC CTATGCCTTA TGTTCCTTAC CCCCCTGCTA CCGAGGTCTA TGTCCGATCG	900
ATCTTCGGCC CGGGTGGCAC CCCTTCCTTA TTCCCAACCT CATGCTCCAC TAAGTCGACC	960
TTCCATGCTG TCCCTGCCCA TATTTGGGAC CGTCTTATGC TGTTCGGGGC CACCTTGGAT	1020
GACCAAGCCT TTTGCTGCTC CCGTTTAATG ACCTACCTTC GCGGCATTAG CTACAAGGTC	1080
ACTGTTGGTA CCCTTGTTGGC TAATGAAGGC TGGAATGCCT CTGAGGACGC CCTCACAGCT	1140
GTTATCACTG CCGCCTACCT TACCATTGTC CACCAGCGGT ATCTCCGCAC CCAGGCTATA	1200
TCCAAGGGGA TGCGTCGTCT GGAACGGGAG CATGCCCAGA AGTTTATAAC ACGCCTCTAC	1260
AGCTGGCTCT TCGAGAAGTC CGGCCGTGAT TACATCCCTG GCCGTCAGTT GGAGTTCTAC	1320
GCCCAGTGCA GCGCTGGCT CTCCGCCGGC TTTCATCTTG ATCCACGGGT GTTGGTTTTT	1380
GACGAGTCGG CCCCCTGCCA TTGTAGGACC GCGATCCGTA AGGCGCTCTC AAAGTTTTGC	1440
TGCTTCATGA AGTGGCTTGG TCAGGAGTGC ACCTGCTTCC TTCAGCCTGC AGAAGGCGCC	1500
GTCGGCGACC AGGGTCATGA TAATGAAGCC TATGAGGGGT CCGATGTTGA CCCTGCTGAG	1560

TCCGCCATTA GTGACATATC TGGGTCCTAT GTCGTCCCTG GCACTGCCCT CCAACCGCTC	1620
TACCAGGCCC TCGATCTCCC CGCTGAGATT GTGGCTCGCG CGGGCCGGCT GACCGCCACA	1680
GTAAAGGTCT CCCAGGTCGA TGGGCGGATC GATTGCGAGA CCCTTCTTGG TAACAAAACC	1740
TTTCGCACGT CGTTCGTTGA CGGGGCGGTC TTAGAGACCA ATGGCCCAGA GCGCCACAAT	1800
CTCTCCTTCG ATGCCAGTCA GAGCACTATG GCCGCTGGCC CTTTCAGTCT CACCTATGCC	1860
GCCTCTGCAG CTGGGCTGGA GGTGCGCTAT GTTGCTGCCG GGCTTGACCA TCGGGCGGTT	1920
TTTGCCCCCG GTGTTTCACC CCGGTCAGCC CCCGGCGAGG TTACCGCCTT CTGCTCTGCC	1980
CTATACAGGT TTAACCGTGA GGCCAGCGC CATTCGCTGA TCGGTAACCT ATGGTTCCAT	2040
CCTGAGGGAC TCATTGGCCT CTTGCCCCG TTTTCGCCCC GGCATGTTTG GGAGTCGGCT	2100
AATCCATTCT GTGGCGAGAG CACACTTTAC ACCCGTACTT GGTCGGAGGT TGATGCCGTC	2160
TCTAGTCCAG CCCGGCCTGA CTTAGGTTTT ATGTCTGAGC CTTCTATACC TAGTAGGGCC	2220
GCCACGCCA CCCTGGCGGC CCCTCTACCC CCCCTGCAC CGGACCCTTC CCCCCCTCCC	2280
TCTGCCCCCG CGCTTGCTGA GCCGGCTTCT GGCCTACCG CCGGGGCCCC GGCCATAACT	2340
CACCAGACGG CCCGGCACCG CCGCCTGCTC TTCACCTACC CGGATGGCTC TAAGGTATTC	2400
GCCGGCTCGC TGTTCGAGTC GACATGCACG TGGCTCGTTA ACGCGTCTAA TGTTGACCAC	2460
CGCCCTGGCG GCGGGCTTTG CCATGCATTT TACCAAAGGT ACCCGCCTC CTTTGATGCT	2520
GCCTCTTTTG TGATGCGCGA CGGCGCGGCC GCGTACACAC TAACCCCCCG GCCAATAATT	2580
CACGCTGTCG CCCCTGATTA TAGGTTGGAA CATAACCCAA AGAGGCTTGA GGCTGCTTAT	2640
CGGGAACTT GCTCCCGCCT CGGCACCGCT GCATAACCCG TCCTCGGGAC CGGCATATAC	2700
CAGGTGCCGA TCGGCCCCAG TTTTGACGCC TGGGAGCGGA ACCACCGCCC CGGGGATGAG	2760
TTGTACCTTC CTGAGCTTGC TGCCAGATGG TTTGAGGCCA ATAGGCCGAC CCGCCCGACT	2820
CTCACTATAA CTGAGGATGT TGCACGGACA GCGAATCTGG CCATCGAGCT TGA CTAGGCC	2880
ACAGATGTCG GCCGGGCTTG TGCCGGCTGT CGGGTCACCC CCGGCGTTGT TCAGTACCAG	2940
TTTACTGCAG GTGTGCCTGG ATCCGGCAAG TCCCCTCTA TCACCCAAGC CGATGTGGAC	3000
GTTGTCGTGG TCCCGACGCG TGAGTTGCGT AATGCCTGGC GCCGTCGCGG CTTTGCTGCT	3060
TTTACCCCGC ATACTGCCGC CAGAGTCACC CAGGGGCGCC GGGTTGTCAT TGATGAGGCT	3120
CCATCCCTCC CCCCTCACCT GCTGCTGCTC CACATGCAGC GGGCCGCCAC CGTCCACCTT	3180
CTTGCGGACC CGAACCAGAT CCCAGCCATC GACTTTGAGC ACGCTGGGCT CGTCCCGCC	3240
ATCAGGCCCC ACTTAGGCCC CACCTCCTGG TGGCATGTTA CCCATCGCTG GCCTGCGGAT	3300
GTATGCGAGC TCATCCGTGG TGCATACCCC ATGATCCAGA CCACTAGCCG GGTTCTCCGT	3360
TCGTTGTTCT GGGGTGAGCC TGCCGTCGGG CAGAACTAG TGTTCACCCA GGCGGCCAAG	3420

CCCGCCAACC	CCGGCTCAGT	GACGGTCCAC	GAGGCGCAGG	GCGCTACCTA	CACGGAGACC	3480
ACTATTATTG	CCACAGCAGA	TGCCCCGGGC	CTTATTCAGT	CGTCTCGGGC	TCATGCCATT	3540
GTTGCTCTGA	CGCGCCACAC	TGAGAAGTGC	GTCATCATTG	ACGCACCAGG	CCTGCTTCGC	3600
GAGGTGGGCA	TCTCCGATGC	AATCGTTAAT	AACTTTTTCC	TCGCTGGTGG	CGAAATTGGT	3660
CACCAGCGCC	CATCAGTTAT	TCCCCTGGC	AACCCTGACG	CCAATGTTGA	CACCCTGGCT	3720
GCCTTCCCGC	CGTCTTGCCA	GATTAGTGCC	TTCCATCAGT	TGGCTGAGGA	GCTTGGCCAC	3780
AGACCTGTCC	CTGTTGCAGC	TGTTCTACCA	CCCTGCCCCG	AGCTCGAACA	GGGCCTTCTC	3840
TACCTGCCCC	AGGAGCTCAC	CACCTGTGAT	AGTGTGCTAA	CATTTGAATT	AACAGACATT	3900
GTGCACTGCC	GCATGGCCGC	CCCAGCCAG	CGCAAGGCCG	TGCTGTCCAC	ACTCGTGGGC	3960
CGCTACGGCG	GTCGCACAAA	GCTCTACAAT	GCTTCCCACT	CTGATGTTTCG	CGACTCTCTC	4020
GCCCCGTTTTA	TCCCGGCCAT	TGGCCCCGTA	CAGGTTACAA	CTTGTGAATT	GTACGAGCTA	4080
GTGGAGGCCA	TGGTCGAGAA	GGGCCAGGAT	GGCTCCGCCG	TCCTTGAGCT	TGATCTTTGC	4140
AACCGTGACG	TGTCCAGGAT	CACCTTCTTC	CAGAAAGATT	GTAACAAGTT	CACCACAGGT	4200
GAGACCATTG	CCCATGGTAA	AGTGGGCCAG	GGCATCTCGG	CCTGGAGCAA	GACCTTCTGC	4260
GCCCTCTTTG	GCCCTTG GTT	CCGCGCTATT	GAGAAGGCTA	TTCTGGCCCT	GCTCCCTCAG	4320
GGTGTGTTTT	ACGGTGATGC	CTTTGATGAC	ACCGTCTTCT	CGGCGGCTGT	GGCCGCAGCA	4380
AAGGCATCCA	TGGTGTTTGA	GAATGACTTT	TCTGAGTTTG	ACTCCACCCA	GAATAACTTT	4440
TCTCTGGGTC	TAGAGTGTGC	TATTATGGAG	GAGTGTGGGA	TGCCGCAGTG	GCTCATCCGC	4500
CTGTATCACC	TTATAAGGTC	TGCGTGGATC	TTGCAGGCCC	CGAAGGAGTC	TCTGCGAGGG	4560
TTTTGGAAGA	AACACTCCGG	TGAGCCCGGC	ACTCTTCTAT	GGAATACTGT	CTGGAATATG	4620
GCCGTTATTA	CCCACTGTTA	TGACTTCCGC	GATTTTCAGG	TGGCTGCCTT	TAAAGGTGAT	4680
GATTCGATAG	TGCTTTGCAG	TGAGTATCGT	CAGAGTCCAG	GAGCTGCTGT	CCTGATCGCC	4740
GGCTGTGGCT	TGAAGTTGAA	GGTAGATTTT	CGCCCGATCG	GTTTGTATGC	AGGTGTTGTG	4800
GTGGCCCCCG	GCCTTGCGC	GCTCCCTGAT	GTTGTGCGCT	TCGCCGGCCG	GCTTACCGAG	4860
AAGAATTGGG	GCCCTGGCCC	TGAGCGGGCG	GAGCAGCTCC	GCCTCGCTGT	TAGTGATTTT	4920
CTCCGCAAGC	TCACGAATGT	AGCTCAGATG	TGTGTGGATG	TTGTTTCCCC	TGTTTATGGG	4980
GTTTCCCCTG	GACTCGTTCA	TAACCTGATT	GGCATGCTAC	AGGCTGTTGC	TGATGGCAAG	5040
GCACATTTCA	CTGAGTCAGT	AAAACCAGTG	CTCGACTTGA	CAAATTCAAT	CTTGTGTCGG	5100
GTGGAATGAA	TAACATGTCT	TTTGCTGCGC	CCATGGGTTC	GCGACCATGC	GCCCTCGGCC	5160
TATTTTGTTG	CTGCTCCTCA	TGTTTTTGCC	TATGCTGCCC	GCGCCACCGC	CCGGTCAGCC	5220
GTCTGGCCGC	CGTCGTGGGC	GGCGCAGCGG	CGGTTCCGGC	GGTGGTTTCT	GGGGTGACCG	5280

GGTTGATTCT CAGCCCTTCG CAATCCCCTA TATTCATCCA ACCAACCCTT TCGCCCCCGA	5340
TGTCACCGCT GCGGCCGGGG CTGGACCTCG TGTTCCGCAA CCCGCCCGAC CACTCGGCTC	5400
CGCTTGCGT GACCAGGCC AGCGCCCCGC CGTTGCCTCA CGTCGTAGAC CTACCACAGC	5460
TGGGGCCGCG CCGCTAACCG CGGTCGCTCC GGCCCATGAC ACCCCGCCAG TGCCTGATGT	5520
CGACTCCCGC GCGCCATCT TCGCCGGCA GTATAACCTA TCAACATCTC CCCTTACCTC	5580
TTCCGTGGCC ACCGGCACTA ACCTGGTTCT TTATGCCGCC CCTCTTAGTC CGCTTTTACC	5640
CCTTCAGGAC GGCACCAATA CCCATATAAT GGCCACGGAA GCTTCTAATT ATGCCAGTA	5700
CCGGGTTGCC CGTGCCACAA TCCGTTACCG CCCGCTGGTC CCCAATGCTG TCGGCGGTTA	5760
CGCCATCTCC ATCTCATTCT GGCCACAGAC CACCACCACC CCGACGTCCG TTGATATGAA	5820
TTCAATAACC TCGACGGATG TTCGTATTTT AGTCCAGCCC GGCATAGCCT CTGAGCTTGT	5880
GATCCCAAGT GAGCGCCTAC ACTATCGTAA CCAAGGCTGG CGCTCCGTCG AGACCTCTGG	5940
GGTGGCTGAG GAGGAGGCTA CCTCTGGTCT TGTTATGCTT TGCATACATG GCTCACTCGT	6000
AAATTCCTAT ACTAATACAC CCTATACCGG TGCCCTCGGG CTGTTGGACT TTGCCCTTGA	6060
GCTTGAGTTT CGCAACCTTA CCCCCGGTAA CACCAATACG CGGGTCTCCC GTTATTCCAG	6120
CACTGCTCGC CACCGCCTTC GTCGCGGTGC GGACGGGACT GCCGAGCTCA CCACCACGGC	6180
TGCTACCCGC TTTATGAAGG ACCTCTATTT TACTAGTACT AATGGTGTCG GTGAGATCGG	6240
CCGCGGGATA GCCCTCACCC TGTTCAACCT TGCTGACACT CTGCTTGGCG GCCTGCCGAC	6300
AGAATTGATT TCGTCGGCTG GTGGCCAGCT GTTCTACTCC CGTCCCGTTG TCTCAGCCAA	6360
TGGCGAGCCG ACTGTAAAGT TGTATACATC TGTAGAGAAT GCTCAGCAGG ATAAGGGTAT	6420
TGCAATCCCG CATGACATTG ACCTCGGAGA ATCTCGTGTG GTTATTCAGG ATTATGATAA	6480
CCAACATGAA CAAGATCGGC CGACGCCTTC TCCAGCCCCA TCGCGCCCTT TCTCTGTCTT	6540
TCGAGCTAAT GATGTGCTTT GGCTCTCTCT CACCGCTGCC GAGTATGACC AGTCCACTTA	6600
TGGCTCTTCG ACTGGCCCAG TTTATGTTTC TGA CTCTGTG ACCTTGGTTA ATGTTGCGAC	6660
CGGCGCGCAG GCCGTTGCCC GGTCGCTCGA TTGGACCAAG GTCACACTTG ACGGTCGCCC	6720
CCTCTCCACC ATCCAGCAGT ACTCGAAGAC CTTCTTTGTC CTGCCGCTCC GCGGTAAGCT	6780
CTCTTTCTGG GAGGCAGGCA CAACTAAAGC CGGGTACCCT TATAATTATA ACACCACTGC	6840
TAGCGACCAA CTGCTTGTCG AGAATGCCGC CGGGCACCGG GTCGCTATTT CCACTTACAC	6900
CACTAGCCTG GGTGCTGGTC CCGTCTCCAT TTCTGCGGTT GCCGTTTTAG CCCCCACTC	6960
TGCGCTAGCA TTGCTTGAGG ATACCTTGGA CTACCCTGCC CGCGCCATA CTTTTGATGA	7020
TTTCTGCCCA GAGTGCCGCC CCCTTGGCCT TCAGGGCTGC GCTTTCCAGT CTACTGTCGC	7080
TGAGCTTCAG CGCCTTAAGA TGAAGGTGGG TAAAACTCGG GAGTTGTAGT TTATTTGCTT	7140

GTGCCCCCCT TCTTTCTGTT GCTTATTCT CATTTCTGCG TTCCGCGCTC CCTGA

7195

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1693 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Glu	Ala	His	Gln	Phe	Ile	Lys	Ala	Pro	Gly	Ile	Thr	Thr	Ala	Ile	1	5	10	15
Glu	Gln	Ala	Ala	Leu	Ala	Ala	Ala	Asn	Ser	Ala	Leu	Ala	Asn	Ala	Val	20	25	30	
Val	Val	Arg	Pro	Phe	Leu	Ser	His	Gln	Gln	Ile	Glu	Ile	Leu	Ile	Asn	35	40	45	
Leu	Met	Gln	Pro	Arg	Gln	Leu	Val	Phe	Arg	Pro	Glu	Val	Phe	Trp	Asn	50	55	60	
His	Pro	Ile	Gln	Arg	Val	Ile	His	Asn	Glu	Leu	Glu	Leu	Tyr	Cys	Arg	65	70	75	80
Ala	Arg	Ser	Gly	Arg	Cys	Leu	Glu	Ile	Gly	Ala	His	Pro	Arg	Ser	Ile	85	90	95	
Asn	Asp	Asn	Pro	Asn	Val	Val	His	Arg	Cys	Phe	Leu	Arg	Pro	Val	Gly	100	105	110	
Arg	Asp	Val	Gln	Arg	Trp	Tyr	Thr	Ala	Pro	Thr	Arg	Gly	Pro	Ala	Ala	115	120	125	
Asn	Cys	Arg	Arg	Ser	Ala	Leu	Arg	Gly	Leu	Pro	Ala	Ala	Asp	Arg	Thr	130	135	140	
Tyr	Cys	Leu	Asp	Gly	Phe	Ser	Gly	Cys	Asn	Phe	Pro	Ala	Glu	Thr	Gly	145	150	155	160
Ile	Ala	Leu	Tyr	Ser	Leu	His	Asp	Met	Ser	Pro	Ser	Asp	Val	Ala	Glu	165	170	175	
Ala	Met	Phe	Arg	His	Gly	Met	Thr	Arg	Leu	Tyr	Ala	Ala	Leu	His	Leu	180	185	190	
Pro	Pro	Glu	Val	Leu	Leu	Pro	Pro	Gly	Thr	Tyr	Arg	Thr	Ala	Ser	Tyr	195	200	205	
Leu	Leu	Ile	His	Asp	Gly	Arg	Arg	Val	Val	Val	Thr	Tyr	Glu	Gly	Asp	210	215	220	
Thr	Ser	Ala	Gly	Tyr	Asn	His	Asp	Val	Ser	Asn	Leu	Arg	Ser	Trp	Ile	225	230	235	240
Arg	Thr	Thr	Lys	Val	Thr	Gly	Asp	His	Pro	Leu	Val	Ile	Glu	Arg	Val				

245										250				255			
Arg	Ala	Ile	Gly	Cys	His	Phe	Val	Leu	Leu	Leu	Thr	Ala	Ala	Pro	Glu		
			260				265						270				
Pro	Ser	Pro	Met	Pro	Tyr	Val	Pro	Tyr	Pro	Arg	Ser	Thr	Glu	Val	Tyr		
			275				280						285				
Val	Arg	Ser	Ile	Phe	Gly	Pro	Gly	Gly	Thr	Pro	Ser	Leu	Phe	Pro	Thr		
			290				295						300				
Ser	Cys	Ser	Thr	Lys	Ser	Thr	Phe	His	Ala	Val	Pro	Ala	His	Ile	Trp		
			305				310						315				
Asp	Arg	Leu	Met	Leu	Phe	Gly	Ala	Thr	Leu	Asp	Asp	Gln	Ala	Phe	Cys		
			320				325						330				
Cys	Ser	Arg	Leu	Met	Thr	Tyr	Leu	Arg	Gly	Ile	Ser	Tyr	Lys	Val	Thr		
			335				340						345				
Val	Gly	Thr	Leu	Val	Ala	Asn	Glu	Gly	Trp	Asn	Ala	Ser	Glu	Asp	Ala		
			350				355						360				
Leu	Thr	Ala	Val	Ile	Thr	Ala	Ala	Tyr	Leu	Thr	Ile	Cys	His	Gln	Arg		
			365				370						375				
Tyr	Leu	Arg	Thr	Gln	Ala	Ile	Ser	Lys	Gly	Met	Arg	Arg	Leu	Glu	Arg		
			380				385						390				
Glu	His	Ala	Gln	Lys	Phe	Ile	Thr	Arg	Leu	Tyr	Ser	Trp	Leu	Phe	Glu		
			395				400						405				
Lys	Ser	Gly	Arg	Asp	Tyr	Ile	Pro	Gly	Arg	Gln	Leu	Glu	Phe	Tyr	Ala		
			410				415						420				
Gln	Cys	Arg	Arg	Trp	Leu	Ser	Ala	Gly	Phe	His	Leu	Asp	Pro	Arg	Val		
			425				430						435				
Leu	Val	Phe	Asp	Glu	Ser	Ala	Pro	Cys	His	Cys	Arg	Thr	Ala	Ile	Arg		
			440				445						450				
Lys	Ala	Leu	Ser	Lys	Phe	Cys	Cys	Phe	Met	Lys	Trp	Leu	Gly	Gln	Glu		
			455				460						465				
Cys	Thr	Cys	Phe	Leu	Gln	Pro	Ala	Glu	Gly	Ala	Val	Gly	Asp	Gln	Gly		
			470				475						480				
His	Asp	Asn	Glu	Ala	Tyr	Glu	Gly	Ser	Asp	Val	Asp	Pro	Ala	Glu	Ser		
			485				490						495				
Ala	Ile	Ser	Asp	Ile	Ser	Gly	Ser	Tyr	Val	Val	Pro	Gly	Thr	Ala	Leu		
			500				505						510				
Gln	Pro	Leu	Tyr	Gln	Ala	Leu	Asp	Leu	Pro	Ala	Glu	Ile	Val	Ala	Arg		
			515				520						525				
Ala	Gly	Arg	Leu	Thr	Ala	Thr	Val	Lys	Val	Ser	Gln	Val	Asp	Gly	Arg		
			530				535						540				
Ile	Asp	Cys	Glu	Thr	Leu	Leu	Gly	Asn	Lys	Thr	Phe	Arg	Thr	Ser	Phe		
			545				550						555				
			560				565						570				
			575				580						585				

Val Asp Gly Ala Val Leu Glu Thr Asn Gly Pro Glu Arg His Asn Leu
 580 585 590
 Ser Phe Asp Ala Ser Gln Ser Thr Met Ala Ala Gly Pro Phe Ser Leu
 595 600 605
 Thr Tyr Ala Ala Ser Ala Ala Gly Leu Glu Val Arg Tyr Val Ala Ala
 610 615 620
 Gly Leu Asp His Arg Ala Val Phe Ala Pro Gly Val Ser Pro Arg Ser
 625 630 635 640
 Ala Pro Gly Glu Val Thr Ala Phe Cys Ser Ala Leu Tyr Arg Phe Asn
 645 650 655
 Arg Glu Ala Gln Arg His Ser Leu Ile Gly Asn Leu Trp Phe His Pro
 660 665 670
 Glu Gly Leu Ile Gly Leu Phe Ala Pro Phe Ser Pro Gly His Val Trp
 675 680 685
 Glu Ser Ala Asn Pro Phe Cys Gly Glu Ser Thr Leu Tyr Thr Arg Thr
 690 695 700
 Trp Ser Glu Val Asp Ala Val Ser Ser Pro Ala Arg Pro Asp Leu Gly
 705 710 715 720
 Phe Met Ser Glu Pro Ser Ile Pro Ser Arg Ala Ala Thr Pro Thr Leu
 725 730 735
 Ala Ala Pro Leu Pro Pro Pro Ala Pro Asp Pro Ser Pro Pro Pro Ser
 740 745 750
 Ala Pro Ala Leu Ala Glu Pro Ala Ser Gly Ala Thr Ala Gly Ala Pro
 755 760 765
 Ala Ile Thr His Gln Thr Ala Arg His Arg Arg Leu Leu Phe Thr Tyr
 770 775 780
 Pro Asp Gly Ser Lys Val Phe Ala Gly Ser Leu Phe Glu Ser Thr Cys
 785 790 795 800
 Thr Trp Leu Val Asn Ala Ser Asn Val Asp His Arg Pro Gly Gly Gly
 805 810 815
 Leu Cys His Ala Phe Tyr Gln Arg Tyr Pro Ala Ser Phe Asp Ala Ala
 820 825 830
 Ser Phe Val Met Arg Asp Gly Ala Ala Ala Tyr Thr Leu Thr Pro Arg
 835 840 845
 Pro Ile Ile His Ala Val Ala Pro Asp Tyr Arg Leu Glu His Asn Pro
 850 855 860
 Lys Arg Leu Glu Ala Ala Tyr Arg Glu Thr Cys Ser Arg Leu Gly Thr
 865 870 875 880
 Ala Ala Tyr Pro Leu Leu Gly Thr Gly Ile Tyr Gln Val Pro Ile Gly
 885 890 895
 Pro Ser Phe Asp Ala Trp Glu Arg Asn His Arg Pro Gly Asp Glu Leu
 900 905 910

Tyr Leu Pro Glu Leu Ala Ala Arg Trp Phe Glu Ala Asn Arg Pro Thr
 915 920 925
 Arg Pro Thr Leu Thr Ile Thr Glu Asp Val Ala Arg Thr Ala Asn Leu
 930 935 940
 Ala Ile Glu Leu Asp Ser Ala Thr Asp Val Gly Arg Ala Cys Ala Gly
 945 950 955 960
 Cys Arg Val Thr Pro Gly Val Val Gln Tyr Gln Phe Thr Ala Gly Val
 965 970 975
 Pro Gly Ser Gly Lys Ser Arg Ser Ile Thr Gln Ala Asp Val Asp Val
 980 985 990
 Val Val Val Pro Thr Arg Glu Leu Arg Asn Ala Trp Arg Arg Arg Gly
 995 1000 1005
 Phe Ala Ala Phe Thr Pro His Thr Ala Ala Arg Val Thr Gln Gly Arg
 1010 1015 1020
 Arg Val Val Ile Asp Glu Ala Pro Ser Leu Pro Pro His Leu Leu Leu
 1025 1030 1035 1040
 Leu His Met Gln Arg Ala Ala Thr Val His Leu Leu Gly Asp Pro Asn
 1045 1050 1055
 Gln Ile Pro Ala Ile Asp Phe Glu His Ala Gly Leu Val Pro Ala Ile
 1060 1065 1070
 Arg Pro Asp Leu Gly Pro Thr Ser Trp Trp His Val Thr His Arg Trp
 1075 1080 1085
 Pro Ala Asp Val Cys Glu Leu Ile Arg Gly Ala Tyr Pro Met Ile Gln
 1090 1095 1100
 Thr Thr Ser Arg Val Leu Arg Ser Leu Phe Trp Gly Glu Pro Ala Val
 1105 1110 1115 1120
 Gly Gln Lys Leu Val Phe Thr Gln Ala Ala Lys Pro Ala Asn Pro Gly
 1125 1130 1135
 Ser Val Thr Val His Glu Ala Gln Gly Ala Thr Tyr Thr Glu Thr Thr
 1140 1145 1150
 Ile Ile Ala Thr Ala Asp Ala Arg Gly Leu Ile Gln Ser Ser Arg Ala
 1155 1160 1165
 His Ala Ile Val Ala Leu Thr Arg His Thr Glu Lys Cys Val Ile Ile
 1170 1175 1180
 Asp Ala Pro Gly Leu Leu Arg Glu Val Gly Ile Ser Asp Ala Ile Val
 1185 1190 1195 1200
 Asn Asn Phe Phe Leu Ala Gly Gly Glu Ile Gly His Gln Arg Pro Ser
 1205 1210 1215
 Val Ile Pro Arg Gly Asn Pro Asp Ala Asn Val Asp Thr Leu Ala Ala
 1220 1225 1230
 Phe Pro Pro Ser Cys Gln Ile Ser Ala Phe His Gln Leu Ala Glu Glu

1235	1240	1245
Leu Gly His Arg Pro Val 1250	Pro Val Ala Ala Val 1255	Leu Pro Pro Cys Pro 1260
Glu Leu Glu Gln Gly 1265	Leu Leu Tyr Leu 1270	Pro Gln Glu Leu Thr Thr Cys 1275 1280
Asp Ser Val Val Thr Phe 1285	Glu Leu Thr 1290	Asp Ile Val His Cys Arg Met 1295
Ala Ala Pro Ser Gln Arg Lys 1300	Ala Val Leu Ser Thr 1305	Leu Val Gly Arg 1310
Tyr Gly Gly Arg Thr Lys 1315	Leu Tyr Asn Ala Ser 1320	His Ser Asp Val Arg 1325
Asp Ser Leu Ala Arg Phe 1330	Ile Pro Ala Ile Gly 1335	Pro Val Gln Val Thr 1340
Thr Cys Glu Leu Tyr Glu 1345	Leu Val Glu Ala Met Val 1350 1355	Glu Lys Gly Gln 1360
Asp Gly Ser Ala Val Leu 1365	Glu Leu Asp Leu Cys Asn Arg 1370	Asp Val Ser 1375
Arg Ile Thr Phe Phe Gln 1380	Lys Asp Cys Asn Lys Phe 1385	Thr Thr Gly Glu 1390
Thr Ile Ala His Gly Lys 1395	Val Gly Gln Gly Ile Ser 1400	Ala Trp Ser Lys 1405
Thr Phe Cys Ala Leu Phe 1410	Gly Pro Trp Phe Arg 1415	Ala Ile Glu Lys Ala 1420
Ile Leu Ala Leu Leu Pro 1425	Gln Gly Val Phe Tyr 1430 1435	Gly Asp Ala Phe Asp 1440
Asp Thr Val Phe Ser Ala 1445	Ala Val Ala Ala Lys 1450	Ala Ser Met Val 1455
Phe Glu Asn Asp Phe Ser 1460	Glu Phe Asp Ser Thr 1465	Gln Asn Asn Phe Ser 1470
Leu Gly Leu Glu Cys Ala 1475	Ile Met Glu Glu Cys 1480	Gly Met Pro Gln Trp 1485
Leu Ile Arg Leu Tyr His 1490	Leu Ile Arg Ser Ala 1495	Trp Ile Leu Gln Ala 1500
Pro Lys Glu Ser Leu Arg 1505	Gly Phe Trp Lys 1510	Lys His Ser Gly Glu Pro 1515 1520
Gly Thr Leu Leu Trp Asn 1525	Thr Val Trp Asn Met 1530	Ala Val Ile Thr His 1535
Cys Tyr Asp Phe Arg Asp 1540	Phe Gln Val Ala Ala 1545	Phe Lys Gly Asp Asp 1550
Ser Ile Val Leu Cys Ser 1555	Glu Tyr Arg Gln Ser 1560	Pro Gly Ala Ala Val 1565

Leu Ile Ala Gly Cys Gly Leu Lys Leu Lys Val Asp Phe Arg Pro Ile
 1570 1575 1580
 Gly Leu Tyr Ala Gly Val Val Val Ala Pro Gly Leu Gly Ala Leu Pro
 1585 1590 1595 1600
 Asp Val Val Arg Phe Ala Gly Arg Leu Thr Glu Lys Asn Trp Gly Pro
 1605 1610 1615
 Gly Pro Glu Arg Ala Glu Gln Leu Arg Leu Ala Val Ser Asp Phe Leu
 1620 1625 1630
 Arg Lys Leu Thr Asn Val Ala Gln Met Cys Val Asp Val Val Ser Arg
 1635 1640 1645
 Val Tyr Gly Val Ser Pro Gly Leu Val His Asn Leu Ile Gly Met Leu
 1650 1655 1660
 Gln Ala Val Ala Asp Gly Lys Ala His Phe Thr Glu Ser Val Lys Pro
 1665 1670 1675 1680
 Val Leu Asp Leu Thr Asn Ser Ile Leu Cys Arg Val Glu
 1685 1690

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Arg Pro Arg Pro Ile Leu Leu Leu Leu Leu Met Phe Leu Pro Met
 1 5 10 15
 Leu Pro Ala Pro Pro Pro Gly Gln Pro Ser Gly Arg Arg Arg Gly Arg
 20 25 30
 Arg Ser Gly Gly Ser Gly Gly Gly Phe Trp Gly Asp Arg Val Asp Ser
 35 40 45
 Gln Pro Phe Ala Ile Pro Tyr Ile His Pro Thr Asn Pro Phe Ala Pro
 50 55 60
 Asp Val Thr Ala Ala Ala Gly Ala Gly Pro Arg Val Arg Gln Pro Ala
 65 70 75 80
 Arg Pro Leu Gly Ser Ala Trp Arg Asp Gln Ala Gln Arg Pro Ala Val
 85 90 95
 Ala Ser Arg Arg Arg Pro Thr Thr Ala Gly Ala Ala Pro Leu Thr Ala
 100 105 110
 Val Ala Pro Ala His Asp Thr Pro Pro Val Pro Asp Val Asp Ser Arg
 115 120 125
 Gly Ala Ile Leu Arg Arg Gln Tyr Asn Leu Ser Thr Ser Pro Leu Thr
 130 135 140

Ser Ser Val Ala Thr Gly Thr Asn Leu Val Leu Tyr Ala Ala Pro Leu
 145 150 155 160
 Ser Pro Leu Leu Pro Leu Gln Asp Gly Thr Asn Thr His Ile Met Ala
 165 170 175
 Thr Glu Ala Ser Asn Tyr Ala Gln Tyr Arg Val Ala Arg Ala Thr Ile
 180 185 190
 Arg Tyr Arg Pro Leu Val Pro Asn Ala Val Gly Gly Tyr Ala Ile Ser
 195 200 205
 Ile Ser Phe Trp Pro Gln Thr Thr Thr Thr Pro Thr Ser Val Asp Met
 210 215 220
 Asn Ser Ile Thr Ser Thr Asp Val Arg Ile Leu Val Gln Pro Gly Ile
 225 230 235 240
 Ala Ser Glu Leu Val Ile Pro Ser Glu Arg Leu His Tyr Arg Asn Gln
 245 250 255
 Gly Trp Arg Ser Val Glu Thr Ser Gly Val Ala Glu Glu Glu Ala Thr
 260 265 270
 Ser Gly Leu Val Met Leu Cys Ile His Gly Ser Leu Val Asn Ser Tyr
 275 280 285
 Thr Asn Thr Pro Tyr Thr Gly Ala Leu Gly Leu Leu Asp Phe Ala Leu
 290 295 300
 Glu Leu Glu Phe Arg Asn Leu Thr Pro Gly Asn Thr Asn Thr Arg Val
 305 310 315 320
 Ser Arg Tyr Ser Ser Thr Ala Arg His Arg Leu Arg Arg Gly Ala Asp
 325 330 335
 Gly Thr Ala Glu Leu Thr Thr Thr Ala Ala Thr Arg Phe Met Lys Asp
 340 345 350
 Leu Tyr Phe Thr Ser Thr Asn Gly Val Gly Glu Ile Gly Arg Gly Ile
 355 360 365
 Ala Leu Thr Leu Phe Asn Leu Ala Asp Thr Leu Leu Gly Gly Leu Pro
 370 375 380
 Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro
 385 390 395 400
 Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val
 405 410 415
 Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp
 420 425 430
 Leu Gly Glu Ser Arg Val Val Ile Gln Asp Tyr Asp Asn Gln His Glu
 435 440 445
 Gln Asp Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg Pro Phe Ser Val
 450 455 460

Leu Arg Ala Asn Asp Val Leu Trp Leu Ser Leu Thr Ala Ala Glu Tyr
 465 470 475 480
 Asp Gln Ser Thr Tyr Gly Ser Ser Thr Gly Pro Val Tyr Val Ser Asp
 485 490 495
 Ser Val Thr Leu Val Asn Val Ala Thr Gly Ala Gln Ala Val Ala Arg
 500 505 510
 Ser Leu Asp Trp Thr Lys Val Thr Leu Asp Gly Arg Pro Leu Ser Thr
 515 520 525
 Ile Gln Gln Tyr Ser Lys Thr Phe Phe Val Leu Pro Leu Arg Gly Lys
 530 535 540
 Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr Asn
 545 550 555 560
 Tyr Asn Thr Thr Ala Ser Asp Gln Leu Leu Val Glu Asn Ala Ala Gly
 565 570 575
 His Arg Val Ala Ile Ser Thr Tyr Thr Thr Ser Leu Gly Ala Gly Pro
 580 585 590
 Val Ser Ile Ser Ala Val Ala Val Leu Ala Pro His Ser Ala Leu Ala
 595 600 605
 Leu Leu Glu Asp Thr Leu Asp Tyr Pro Ala Arg Ala His Thr Phe Asp
 610 615 620
 Asp Phe Cys Pro Glu Cys Arg Pro Leu Gly Leu Gln Gly Cys Ala Phe
 625 630 635 640
 Gln Ser Thr Val Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys
 645 650 655
 Thr Arg Glu Leu
 660

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Asn Asn Met Ser Phe Ala Ala Pro Met Gly Ser Arg Pro Cys Ala
 1 5 10 15
 Leu Gly Leu Phe Cys Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys Pro
 20 25 30
 Arg His Arg Pro Val Ser Arg Leu Ala Ala Val Val Gly Gly Ala Ala
 35 40 45
 Ala Val Pro Ala Val Val Ser Gly Val Thr Gly Leu Ile Leu Ser Pro
 50 55 60

Ser Gln Ser Pro Ile Phe Ile Gln Pro Thr Pro Ser Pro Pro Met Ser
65 70 75 80

Pro Leu Arg Pro Gly Leu Asp Leu Val Phe Ala Asn Pro Pro Asp His
85 90 95

Ser Ala Pro Leu Gly Val Thr Arg Pro Ser Ala Pro Pro Leu Pro His
100 105 110

Val Val Asp Leu Pro Gln Leu Gly Pro Arg Arg
115 120

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Composite Mexico strain

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCCATGGAGG CCCACCACTT CATTAAGGCT CCTGGCATCA CTACTGCTAT TGAGCAAGCA	60
GCTCTAGCAG CGGCCAACTC CGCCCTTGCG AATGCTGTGG TGGTCCGGCC TTTCTTTCC	120
CATCAGCAGG TTGAGATCCT TATAAATCTC ATGCAACCTC GGCAGCTGGT GTTTCGTCCT	180
GAGGTTTTTTT GGAATCACCC GATTCAACGT GTTATACATA ATGAGCTTGA GCAGTATTGC	240
CGTGCTCGCT CGGGTCGCTG CCTTGAGATT GGAGCCCACC CACGCTCCAT TAATGATAAT	300
CCTAATGTCC TCCATCGCTG CTTTCTCCAC CCCGTCGGCC GGGATGTTCA GCGCTGGTAC	360
ACAGCCCCGA CTAGGGGACC TGCGGCGAAC TGTCGCCGCT CGGCACTTCG TGGTCTGCCA	420
CCAGCCGACC GCACTTACTG TTTTGATGGC TTTGCCGGCT GCCGTTTTGC CGCCGAGACT	480
GGTGTGGCTC TCTATTCTCT CCATGACTTG CAGCCGGCTG ATGTTGCCGA GGCGATGGCT	540
CGCCACGGCA TGACCCGCCT TTATGCAGCT TTCCACTTGC CTCCAGAGGT GTCCTGCCT	600
CCTGGCACCT ACCGGACATC ATCCTACTTG CTGATCCACG ATGGTAAGCG CGCGGTTGTC	660
ACTTATGAGG GTGACACTAG CGCCGGTTAC AATCATGATG TTGCCACCCCT CCGCACATGG	720
ATCAGGACAA CTAAGGTTGT GGGTGAACAC CCTTTGGTGA TCGAGCGGGT GCGGGGTATT	780
GGCTGTCACT TTGTGTTGTT GATCACTGCG GCCCCTGAGC CCTCCCCGAT GCCCTACGTT	840
CCTTACCCGC GTTCGACGGA GGTCTATGTC CGGTCTATCT TTGGGCCCCG CGGGTCCCCG	900

TCGCTGTTCC CGACCGCTTG TGCTGTCAAG TCCACTTTTC ACGCCGTCCC CACGCACATC	960
TGGGACCGTC TCATGCTCTT TGGGGCCACC CTCGACGACC AGGCCTTTTG CTGCTCCAGG	1020
CTTATGACGT ACCTTCGTGG CATTAGCTAT AAGGTAAC TG GGTGCCCCT GGTGCTAAT	1080
GAAGGCTGGA ATGCCACCGA GGATGCGCTC ACTGCAGTTA TTACGGCGGC TTACCTCACA	1140
ATATGTCATC AGCGTTATTT GCGGACCCAG GCGATTTCTA AGGGCATGCG CCGGCTTGAG	1200
CTTGAACATG CTCAGAAATT TATTTACGC CTCTACAGCT GGCTATTTGA GAAGTCAGGT	1260
CGTGATTACA TCCCAGGCCG CCAGCTGCAG TTCTACGCTC AGTGCCGCCG CTGGTTATCT	1320
GCCGGGTTCC ATCTCGACCC CCGCACCTTA GTTTTTGATG AGTCAGTGCC TTGTAGCTGC	1380
CGAACCACCA TCCGGCGGAT CGCTGGAAAA TTTTGCTGTT TTATGAAGTG GCTCGGTCAG	1440
GAGTGTTCCTT GTTTCCTCCA GCCC GCCGAG GGGCTGGCGG GCGACCAAGG TCATGACAAT	1500
GAGGCCTATG AAGGCTCTGA TGTGATACT GCTGAGCCTG CCACCCTAGA CATTACAGGC	1560
TCATACATCG TGGATGGTCG GTCTCTGCAA ACTGTCTATC AAGCTCTCGA CCTGCCAGCT	1620
GACCTGGTAG CTCGCGCAGC CCGACTGTCT GCTACAGTTA CTGTTACTGA AACCTCTGGC	1680
CGTCTGGATT GCCAAACAAT GATCGGCAAT AAGACTTTTC TCACTACCTT TGTGATGGG	1740
GCACGCCTTG AGGTTAACGG GCCTGAGCAG CTTAACCTCT CTTTTGACAG CCAGCAGTGT	1800
AGTATGGCAG CCGGCCCGTT TTGCCTCACC TATGCTGCCG TAGATGGCGG GCTGGAAGTT	1860
CATTTTTCCA CCGCTGGCCT CGAGAGCCGT GTTGTTCCTC CCCCTGGTAA TGCCCCGACT	1920
GCCCCGCCGA GTGAGGTCAC CGCCTTCTGC TCAGCTCTTT ATAGGCACAA CCGGCAGAGC	1980
CAGCGCCAGT CGGTTATTGG TAGTTTGTGG CTGCACCCTG AAGGTTTGCT CGGCCTGTTC	2040
CCGCCCTTTT CACCCGGGCA TGAGTGGCGG TCTGCTAACC CATTTTGCGG CGAGAGCACG	2100
CTCTACACCC GCACTTGGTC CACAATTACA GACACACCCT TAACTGTCGG GCTAATTTCC	2160
GGTCATTTGG ATGCTGCTCC CCACTCGGGG GGGCCACCTG CTA CTACTGCCAC AGGCCCTGCT	2220
GTAGGCTCGT CTGACTCTCC AGACCCTGAC CCGCTACCTG ATGTTACAGA TGGCTCACGC	2280
CCCTCTGGGG CCCGTCCGGC TGGCCCCAAC CCGAATGGCG TTCCGCAGCG CCGCTTACTA	2340
CACACCTACC CTGACGGCGC TAAGATCTAT GTCGGCTCCA TTTTCGAGTC TGAGTGCACC	2400
TGGCTTGTC ACGCATCTAA CGCCGGCCAC CGCCCTGGTG GCGGGCTTTG TCATGCTTTT	2460
TTTCAGCGTT ACCCTGATTC GTTTGACGCC ACCAAGTTTG TGATGCGTGA TGGTCTTGCC	2520
GCGTATACCC TTACACCCCG GCCGATCATT CATGCGGTGG CCCC GACTA TCGATTGGAA	2580
CATAACCCCA AGAGGCTCGA GGCTGCCTAC CGCGAGACTT GCGCCCGCCG AGGCACTGCT	2640
GCCTATCCAC TCTTAGGCGC TGGCATTAC CAGGTGCCTG TTAGTTGAG TTTTGATGCC	2700
TGGGAGCGGA ACCACGCCG GTTTGACGAG CTTTACCTAA CAGAGCTGGC GGCTCGGTGG	2760

TTTGAATCCA	ACCGCCCCGG	TCAGCCCACG	TTGAACATAA	CTGAGGATAC	CGCCCGTGCG	2820
GCCAACCTGG	CCCTGGAGCT	TGACTCCGGG	AGTGAAGTAG	GCCGCGCATG	TGCCGGGTGT	2880
AAAGTCGAGC	CTGGCGTTGT	GCGGTATCAG	TTTACAGCCG	GTGTCCCCGG	CTCTGGCAAG	2940
TCAAAGTCCG	TGCAACAGGC	GGATGTGGAT	GTTGTTGTTG	TGCCCCACTCG	CGAGCTTCGG	3000
AACGCTTGGC	GGCGCCGGGG	CTTTGCGGCA	TTCACTCCGC	ACACTGCGGC	CCGTGTCACT	3060
AGCGGCCGTA	GGGTTGTCAT	TGATGAGGCC	CCTTCGCTCC	CCCCACACTT	GCTGCTTTTA	3120
CATATGCAGC	GTGCTGCATC	TGTGCACCTC	CTTGGGGACC	CGAATCAGAT	CCCCGCCATA	3180
GATTTTGAGC	ACACCGGTCT	GATTCCAGCA	ATACGGCCGG	AGTTGGTCCC	GACTTCATGG	3240
TGGCATGTCA	CCCACCGTTG	CCCTGCAGAT	GTCTGTGAGT	TAGTCCGTGG	TGCTTACCCT	3300
AAAATCCAGA	CTACAAGTAA	GGTGCTCCGT	TCCCTTTTCT	GGGGAGAGCC	AGCTGTCGGC	3360
CAGAAGCTAG	TGTTACACACA	GGCTGCTAAG	GCCGCGCACC	CCGGATCTAT	AACGGTCCAT	3420
GAGGCCCAGG	GTGCCACTTT	TACCACTACA	ACTATAATTG	CAACTGCAGA	TGCCCCGTGGC	3480
CTCATACAGT	CCTCCCCGGG	TCACGCTATA	GTTGCTCTCA	CTAGGCATAC	TGAAAAATGT	3540
GTTATACTTG	ACTCTCCCGG	CCTGTTGCGT	GAGGTGGGTA	TCTCAGATGC	CATTGTTAAT	3600
AATTTCTTCC	TTTCGGGTGG	CGAGGTGGT	CACCAGAGAC	CATCGGTCAT	TCCGCGAGGC	3660
AACCCTGACC	GCAATGTTGA	CGTGCTTGCG	GCGTTTCCAC	CTTCATGCCA	AATAAGCGCC	3720
TTCCATCAGC	TTGCTGAGGA	GCTGGGCCAC	CGGCCGGCGC	CGGTGGCGGC	TGTGCTACCT	3780
CCCTGCCCTG	AGCTTGAGCA	GGGCCTTCTC	TATCTGCCAC	AGGAGCTAGC	CTCCTGTGAC	3840
AGTGTGTGA	CATTTGAGCT	AACTGACATT	GTGCACTGCC	GCATGGCGGC	CCCTAGCCAA	3900
AGGAAAGCTG	TTTTGTCCAC	GCTGGTAGGC	CGGTATGGCA	GACGCACAAG	GCTTTATGAT	3960
GCGGGTCACA	CCGATGTCCG	CGCCTCCCTT	GCGCGCTTTA	TTCCCACTCT	CGGGCGGGTT	4020
ACTGCCACCA	CCTGTGAACT	CTTTGAGCTT	GTAGAGGCGA	TGGTGGAGAA	GGGCCAAGAC	4080
GGTTCAGCCG	TCCTCGAGTT	GGATTTGTGC	AGCCGAGATG	TCTCCCGCAT	AACCTTTTTT	4140
CAGAAGGATT	GTAACAAGTT	CACGACCGGC	GAGACAATTG	CGCATGGCAA	AGTCGGTCAG	4200
GGTATCTTCC	GCTGGAGTAA	GACGTTTTGT	GCCCTGTTTG	GCCCCTGGTT	CCGTGCGATT	4260
GAGAAGGCTA	TTCTATCCCT	TTTACCACAA	GCTGTGTTCT	ACGGGGATGC	TTATGACGAC	4320
TCAGTATTCT	CTGCTGCCGT	GGCTGGCGCC	AGCCATGCCA	TGGTGTGTTGA	AAATGATTTT	4380
TCTGAGTTTG	ACTCGACTCA	GAATAACTTT	TCCCTAGGTC	TTGAGTGCGC	CATTATGGAA	4440
GAGTGTGGTA	TGCCCCAGTG	GCTTGTGAGG	TTGTACCATG	CCGTCCGGTC	GGCGTGGATC	4500
CTGCAGGCCC	CAAAAGAGTC	TTTGAGAGGG	TTCTGGAAGA	AGCATTCTGG	TGAGCCGGGC	4560
AGCTTGCTCT	GGAATACGGT	GTGGAACATG	GCAATCATTG	CCCATTGCTA	TGAGTTCCGG	4620

GACCTCCAGG	TTGCCGCCTT	CAAGGGCGAC	GACTCGGTCG	TCCTCTGTAG	TGAATACCGC	4680
CAGAGCCCAG	GCGCCGGTTC	GCTTATAGCA	GGCTGTGGTT	TGAAGTTGAA	GGCTGACTTC	4740
CGGCCGATTG	GGCTGTATGC	CGGGGTTGTC	GTCGCCCCGG	GGCTCGGGGC	CCTACCCGAT	4800
GTCGTTGAT	TCGCCGGACG	GCTTTCGGAG	AAGAACTGGG	GGCCTGATCC	GGAGCGGGCA	4860
GAGCAGCTCC	GCCTCGCCGT	GCAGGATTTT	CTCCGTAGGT	TAACGAATGT	GGCCCAGATT	4920
TGTGTTGAGG	TGGTGTCTAG	AGTTTACGGG	GTTTCCCCGG	GTCTGGTTCA	TAACCTGATA	4980
GGCATGCTCC	AGACTATTGG	TGATGGTAAG	GCGCATTTTA	CAGAGTCTGT	TAAGCCTATA	5040
CTTGACCTTA	CACACTCAAT	TATGCACCGG	TCTGAATGAA	TAACATGTGG	TTTGCTGCGC	5100
CCATGGGTTC	GCCACCATGC	GCCCTAGGCC	TCTTTTGCTG	TTGTTCCCTCT	TGTTTCTGCC	5160
TATGTTGCC	GCGCCACCGA	CCGGTCAGCC	GTCTGGCCGC	CGTCGTGGGC	GGCGCAGCGG	5220
CGGTACCGGC	GGTGGTTTCT	GGGGTGACCG	GGTTGATTCT	CAGCCCTTCG	CAATCCCCTA	5280
TATTCATCCA	ACCAACCCCT	TTGCCCCAGA	CGTTGCCGCT	GCGTCCGGGT	CTGGACCTCG	5340
CCTTCGCCAA	CCAGCCCGGC	CACTTGGCTC	CACTTGGCGA	GATCAGGCCC	AGCGCCCCTC	5400
CGCTGCCTCC	CGTCGCCGAC	CTGCCACAGC	CGGGGCTGCG	GCGCTGACGG	CTGTGGCGCC	5460
TGCCCCATGAC	ACCTCACCCG	TCCCGGACGT	TGATTCTCGC	GGTGCAATTC	TACGCCGCCA	5520
GTATAATTTG	TCTACTTCAC	CCCTGACATC	CTCTGTGGCC	TCTGGCACTA	ATTTAGTCCT	5580
GTATGCAGCC	CCCCTTAATC	CGCCTCTGCC	GCTGCAGGAC	GGTACTAATA	CTCACATTAT	5640
GGCCACAGAG	GCCTCCAATT	ATGCACAGTA	CCGGGTTGCC	CGCGCTACTA	TCCGTTACCG	5700
GCCCCTAGTG	CCTAATGCAG	TTGGAGGCTA	TGCTATATCC	ATTTCTTTCT	GGCCTCAAAC	5760
AACCACAACC	CCTACATCTG	TTGACATGAA	TTCCATTACT	TCCACTGATG	TCAGGATTCT	5820
TGTTCAACCT	GGCATAGCAT	CTGAATTGGT	CATCCCAAGC	GAGCGCCTTC	ACTACCGCAA	5880
TCAAGGTTGG	CGCTCGGTTG	AGACATCTGG	TGTTGCTGAG	GAGGAAGCCA	CCTCCGGTCT	5940
TGTCATGTTA	TGCATACATG	GCTCTCCAGT	TAACCTCTAT	ACCAATACCC	CTTATACCGG	6000
TGCCCTTGCC	TTACTGGACT	TTGCCTTAGA	GCTTGAGTTT	CGCAATCTCA	CCACCTGTAA	6060
CACCAATACA	CGTGTGTCCC	GTTACTCCAG	CACTGCTCGT	CACTCCGCCC	GAGGGGCCGA	6120
CGGGACTGCG	GAGCTGACCA	CAACTGCAGC	CACCAGGTTT	ATGAAAGATC	TCCACTTTAC	6180
CGGCCTTAAT	GGGGTAGGTG	AAGTCGGCCG	CGGGATAGCT	CTAACATTAC	TTAACCTTGC	6240
TGACACGCTC	CTCGGCGGGC	TCCCGACAGA	ATTAATTTCT	TCGGCTGGCG	GGCAACTGTT	6300
TTATTCCCGC	CCGGTTGTCT	CAGCCAATGG	CGAGCCAACC	GTGAAGCTCT	ATACATCAGT	6360
GGAGAATGCT	CAGCAGGATA	AGGGTGTTGC	TATCCCCCAC	GATATCGATC	TTGGTGATTC	6420
GCGTGTGGTC	ATTCAGGATT	ATGACAACCA	GCATGAGCAG	GATCGGCCCCA	CCCCGTGCGC	6480

TGCGCCATCT CGGCCTTTTT CTGTTCTCCG AGCAAATGAT GTACTTTGGC TGTCCCTCAC	6540
TGCAGCCGAG TATGACCACT CCACTTACGG GTCGTCAACT GGCCCGGTTT ATATCTCGGA	6600
CAGCGTGACT TTGGTGAATG TTGCGACTGG CGCGCAGGCC GTAGCCCGAT CGCTTGACTG	6660
GTCCAAAGTC ACCCTCGACG GCGGGCCCCCT CCCGACTGTT GAGCAATATT CCAAGACATT	6720
CTTTGTGCTC CCCCTTCGTG GCAAGCTCTC CTTTTGGGAG GCCGGCACAA CAAAAGCAGG	6780
TTATCCTTAT AATTATAATA CTAAGCTAG TGACCAGATT CTGATTGAAA ATGCTGCCGG	6840
CCATCGGGTC GCCATTTCAA CCTATACCAC CAGGCTTGGG GCCGGTCCGG TCGCCATTTT	6900
TGCGGCCGCG GTTTTGGCTC CACGCTCCGC CCTGGCTCTG CTGGAGGATA CTTTTGATTA	6960
TCCGGGGCGG GCGCACACAT TTGATGACTT CTGCCCTGAA TGCCGCGCTT TAGGCCTCCA	7020
GGGTTGTGCT TTCCAGTCAA CTGTCGCTGA GCTCCAGCGC CTTAAAGTTA AGGTGGGTAA	7080
AACTCGGGAG TTGTAGTTTA TTTGGCTGTG CCCACCTACT TATATCTGCT GATTTCCCTT	7140
ATTTCTTTTT TCTCGGTCCC GCGCTCCCTG A	7171

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1575 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: T: Mexican strain

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTTGCGTGAG GTGGGTATCT CAGATGCCAT TGTTAATAAT TTCTTCCTTT CGGGTGGCGA	60
GGTTGGTCAC CAGAGACCAT CGGTCATTCC GCGAGGCAAC CCTGACCGCA ATGTTGACGT	120
GCTTGCGGCG TTTCCACCTT CATGCCAAAT AAGCGCCTTC CATCAGCTTG CTGAGGAGCT	180
GGGCCACCGG CCGGCGCCGG TGGCGGCTGT GCTACCTCCC TGCCCTGAGC TTGAGCAGGG	240
CCTTCTCTAT CTGCCACAGG AGCTAGCCTC CTGTGACAGT GTTGTGACAT TTGAGCTAAC	300
TGACATTGTG CACTGCCGCA TGGCGGCCCC TAGCCAAAGG AAAGCTGTTT TGTCCACGCT	360
GGTAGGCCGG TATGGCAGAC GCACAAGGCT TTATGATGCG GGTCACACCG ATGTCCGCGC	420
CTCCCTTGCG CGCTTTATTC CCACTCTCGG GCGGGTTACT GCCACCACCT GTGAACTCTT	480
TGAGCTTGTA GAGGCGATGG TGGAGAAGGG CCAAGACGGT TCAGCCGTCC TCGAGTTGGA	540

TTTGTGCAGC CGAGATGTCT CCCGCATAAC CTTTTTCCAG AAGGATTGTA ACAAGTTCAC	600
GACCGGCGAG ACAATTGCGC ATGGCAAAGT CGGTCAGGGT ATCTTCCGCT GGAGTAAGAC	660
CTTTTGTGCC CTGTTTGGCC CCTGGTTCCG TGCATTGAG AAGGCTATTC TATCCCTTTT	720
ACCACAAGCT GTGTTCTACG GGGATGCTTA TGACGACTCA GTATTCTCTG CTGCCGTGGC	780
TGGCGCCAGC CATGCCATGG TGTTTGAAAA TGATTTTCT GAGTTTGA CTGACTCAGAA	840
TAACTTTTCC CTAGGTCTTG AGTGCGCCAT TATGGAAGAG TGTGGTATGC CCCAGTGGCT	900
TGTCAGGTTG TACCATGCCG TCCGGTCGGC GTGGATCCTG CAGGCCCAA AAGAGTCTTT	960
GAGAGGGTTC TGGAAGAAGC ATTCTGGTGA GCCGGGCACG TTGCTCTGGA ATACGGTGTG	1020
GAACATGGCA ATCATTGCCC ATTGCTATGA GTTCCGGGAC CTCCAGGTTG CCGCCTTCAA	1080
GGGCGACGAC TCGGTCGTCC TCTGTAGTGA ATACCGCCAG AGCCCAGGCG CCGGTTTCGCT	1140
TATAGCAGGC TGTGGTTTGA AGTTGAAGGC TGA CTTCGG CCGATTGGGC TGTATGCCGG	1200
GGTTGTTCGTC GCCCCGGGGC TCGGGGCCCT ACCCGATGTC GTTCGATTGC CCGGACGGCT	1260
TTCGGAGAAG AACTGGGGGC CTGATCCGGA GCGGGCAGAG CAGCTCCGCC TCGCCGTGCA	1320
GGATTTCCTC CGTAGGTTAA CGAATGTGGC CCAGATTTGT GTTGAGGTGG TGTCTAGAGT	1380
TTACGGGGTT TCCCCGGGTC TGGTTCATAA CCTGATAGGC ATGCTCCAGA CTATTGGTGA	1440
TGGTAAGGCG CATTTTACAG AGTCTGTAA GCCTATACTT GACCTTACAC ACTCAATTAT	1500
GCACCGGTCT GAATGAATAA CATGTGGTTT GCTGCGCCA TGGGTTGCC ACCATGCGCC	1560
CTAGGCCTCT TTTGC	1575

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 874 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Tashkent strain

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGGGCCCCGT ACAGGTCACA ACCTGTGAGT TGTACGAGCT AGTGGAGGCC ATGGTCGAGA	60
AAGGCCAGGA TGGCTCCGCC GTCCTTGAGC TCGATCTCTG CAACCGTGAC GTGTCCAGGA	120
TCACCTTTTT CCAGAAAGAT TGCAATAAGT TCACCACGGG AGAGACCATC GCCCATGGTA	180


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AAGTGGGCCA GGGCATTTCG GCCTGGAGTA AGACCTTCTG TGCCCTTTTC GGCCCCTGGT      240
TCCGTGCTAT TGAGAAGGCT ATTCTGGCCC TGCTCCCTCA GGGTGTGTTT TATGGGGATG      300
CCTTTGATGA CACCGTCTTC TCGGCGCGTG TGGCCGCAGC AAAGGCGTCC ATGGTGTTTG      360
AGAATGACTT TTCTGAGTTT GACTCCACCC AGAATAATTT TTCCCTGGGC CTAGAGTGTG      420
CTATTATGGA GAAGTGTGGG ATGCCGAAGT GGCTCATCCG CTTGTACCAC CTTATAAGGT      480
CTGCGTGGAT CCTGCAGGCC CCGAAGGAGT CCCTGCGAGG GTGTTGGAAG AAACACTCCG      540
GTGAGCCCGG CACTCTTCTA TGGAATACTG TCTGGAACAT GGCCGTTATC ACCCATTGTT      600
ACGATTTCG CGATTTGCAG GTGGCTGCCT TTAAAGGTGA TGATTCGATA GTGCTTTGCA      660
GTGAGTACCG TCAGAGTCCA GGGGCTGCTG TCCTGATTGC TGGCTGTGGC TTAAAGCTGA      720
AGGTGGGTTT CCGTCCGATT GTTTGTATG CAGGTGTTGT GGTGACCCCC GGCCTTGCGG      780
CGCTTCCCGA CGTCGTGCGC TTGTCCGGCC GGCTTACTGA GAAGAATTGG GGCCCTGGCC      840
CTGAGCGGGC GGAGCAGCTC CGCCTTGCTG TGCG                                  874

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(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Clone 406.4-2 cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

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C GCC AAC CAG CCC GGC CAC TTG GCT CCA CTT GGC GAG ATC AGG CCC      46
Ala Asn Gln Pro Gly His Leu Ala Pro Leu Gly Glu Ile Arg Pro
  1             5             10             15

AGC GCC CCT CCG CTG CCT CCC GTC GCC GAC CTG CCA CAG CCG GGG CTG      94
Ser Ala Pro Pro Leu Pro Pro Val Ala Asp Leu Pro Gln Pro Gly Leu
             20             25             30

CGG CGC TGACGGCTGT GGCGCCTGCC CATGACACCT CACCCGTCCC GGACGTTGAT      150
Arg Arg

TCTCGCGGTG CAATTCTACG CCGCCAGTAT AATTTGTCTA CTTACCCCT GACATCCTCT      210

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GTGGCCTCTG GCACTAATTT AGTCCTGTAT GCAGCCCCC TTAATCCGCC TCTGCCGCTG 270
 CAGGACGGTA CTAATACTCA CATTATGGCC ACAGAGGCCT CCAATTATGC ACAGTACCGG 330
 GTTGCCCGCG CTACTATCCG TTACCGGCCC CTAGTGCCTA ATGCAGTTGG AGGCTATGCT 390
 ATATCCATTT CTTTCTGGCC TCAAACAACC ACAACCCCTA CATCTGTTGA CATGAATTC 449

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ala Asn Gln Pro Gly His Leu Ala Pro Leu Gly Glu Ile Arg Pro Ser
 1 5 10 15
 Ala Pro Pro Leu Pro Pro Val Ala Asp Leu Pro Gln Pro Gly Leu Arg
 20 25 30
 Arg

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 130 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (C) INDIVIDUAL ISOLATE: Clone 406.3-2

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 5..130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGAT ACT TTT GAT TAT CCG GGG CGG GCG CAC ACA TTT GAT GAC TTC TGC 49
 Thr Phe Asp Tyr Pro Gly Arg Ala His Thr Phe Asp Asp Phe Cys
 1 5 10 15
 CCT GAA TGC CGC GCT TTA GGC CTC CAG GGT TGT GCT TTC CAG TCA ACT 97
 Pro Glu Cys Arg Ala Leu Gly Leu Gln Gly Cys Ala Phe Gln Ser Thr
 20 25 30
 GTC GCT GAG CTC CAG CGC CTT AAA GTT AAG GTT 130

Val Ala Glu Leu Gln Arg Leu Lys Val Lys Val
35 40

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Thr Phe Asp Tyr Pro Gly Arg Ala His Thr Phe Asp Asp Phe Cys Pro
1 5 10 15
Glu Cys Arg Ala Leu Gly Leu Gln Gly Cys Ala Phe Gln Ser Thr Val
20 25 30
Ala Glu Leu Gln Arg Leu Lys Val Lys Val
35 40

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: 406.4-2 epitope - Mexican strain

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Ala Asn Gln Pro Gly His Leu Ala Pro Leu Gly Glu Ile Arg Pro Ser
1 5 10 15
Ala Pro Pro Leu Pro Pro Val Ala Asp Leu Pro Gln Pro Gly Leu Arg
20 25 30
Arg

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (C) INDIVIDUAL ISOLATE: 406.4-2 epitope - Burma strain
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ala	Asn	Pro	Pro	Asp	His	Ser	Ala	Pro	Leu	Gly	Val	Thr	Arg	Pro	Ser
1				5					10					15	
Ala	Pro	Pro	Leu	Pro	His	Val	Val	Asp	Leu	Pro	Gln	Leu	Gly	Pro	Arg
			20					25					30		
Arg															

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (C) INDIVIDUAL ISOLATE: 406.3-2 epitope - Mexican strain
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Thr	Phe	Asp	Tyr	Pro	Gly	Arg	Ala	His	Thr	Phe	Asp	Asp	Phe	Cys	Pro
1				5					10					15	
Glu	Cys	Arg	Ala	Leu	Gly	Leu	Gln	Gly	Cys	Ala	Phe	Gln	Ser	Thr	Val
			20					25					30		
Ala	Glu	Leu	Gln	Arg	Leu	Lys	Val	Lys	Val						
			35				40								

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: 406.3-2 epitope - Burma strain

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Thr	Leu	Asp	Tyr	Pro	Ala	Arg	Ala	His	Thr	Phe	Asp	Asp	Phe	Cys	Pro
1				5					10					15	

Glu	Cys	Arg	Pro	Leu	Gly	Leu	Gln	Gly	Cys	Ala	Phe	Gln	Ser	Thr	Val
			20					25					30		

Ala	Glu	Leu	Gln	Arg	Leu	Lys	Met	Lys	Val
		35					40		